

DESIGN OF SYNTHETIC DNA PROBES.

1 2 3 4 5 6 7 8 9 10 11 12 13 14 15
A. M - N - P - N - N - R - S - E - H - D - T - I - K - T - T
ATG AAT CCN AAT AAT CGN TCN GAA CAT GAT ACN ATT AAA ACN ACN
C C C AGA AGT G C C C G
G C A

B. ATGAATCCTAATAATCG
C C C C
A
G

C. GAACATGATACAATTAA
G C C G C
A

FOTEC 80 "ZG 35416 0

- A. PROTEIN SEQUENCE OF THE N-TERMINI OF PEAKS A AND B OF THE B.T.T. TOXIN AND DEDUCED DNA SEQUENCE.
- B. SYNTHETIC A1 PROBE, 32-FOLD DEGENERATE 17-MER, BASED ON AMINO ACIDS 1-6.
- C. SYNTHETIC A2 PROBE, 48-FOLD DEGENERATE 17-MER, BASED ON AMINO ACIDS 8-13.

FIG.1

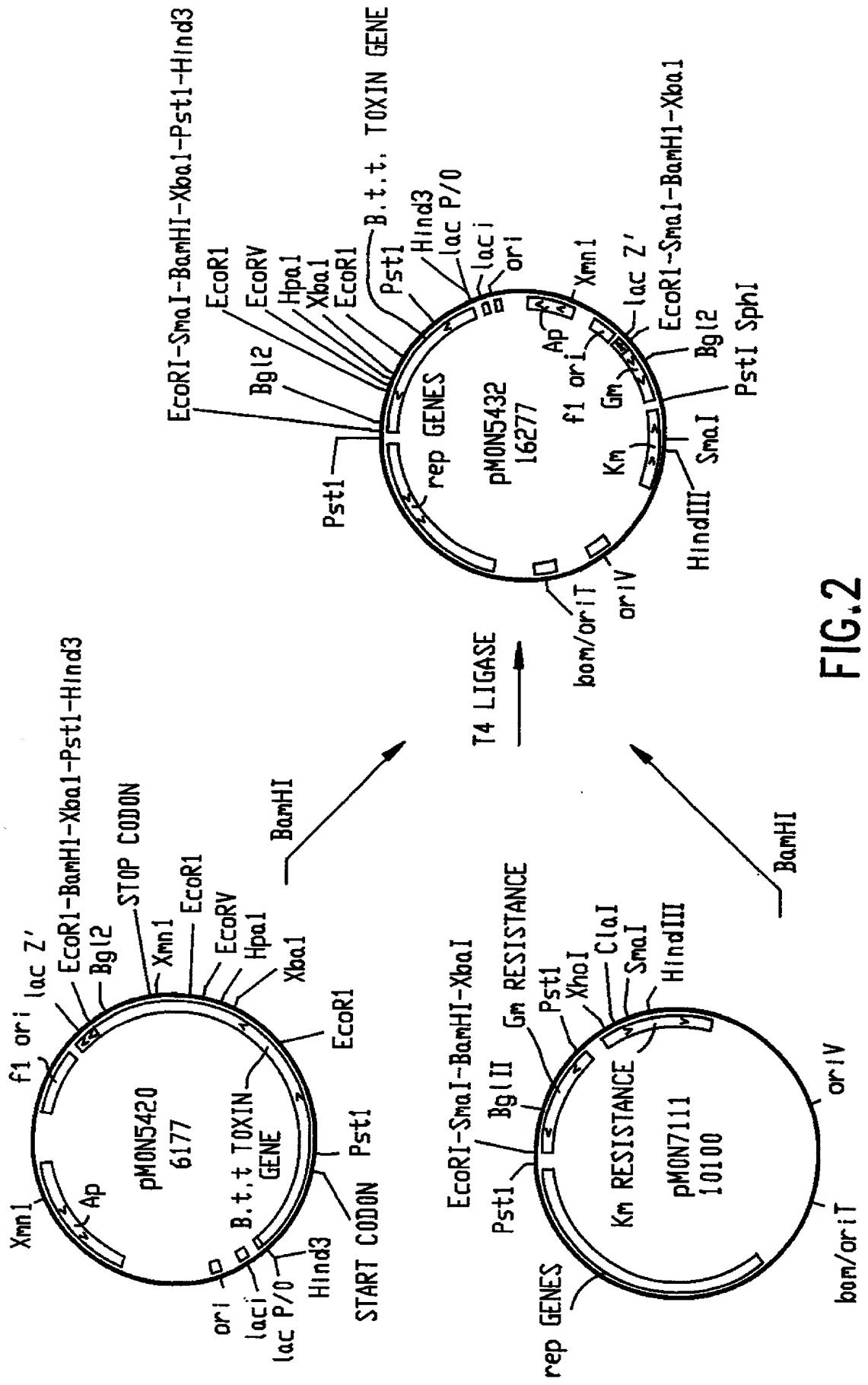


FIG.2

FIG. 3

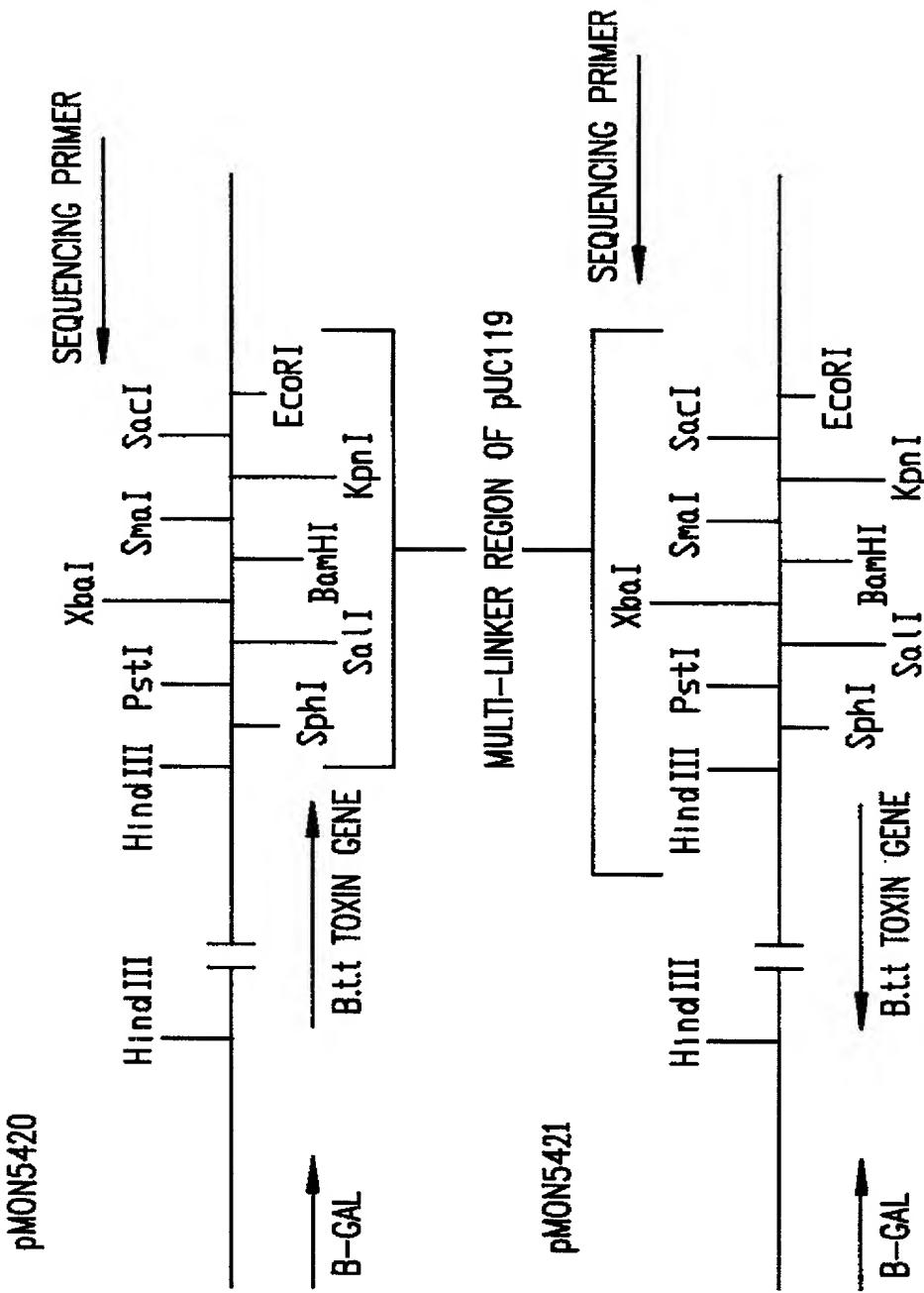
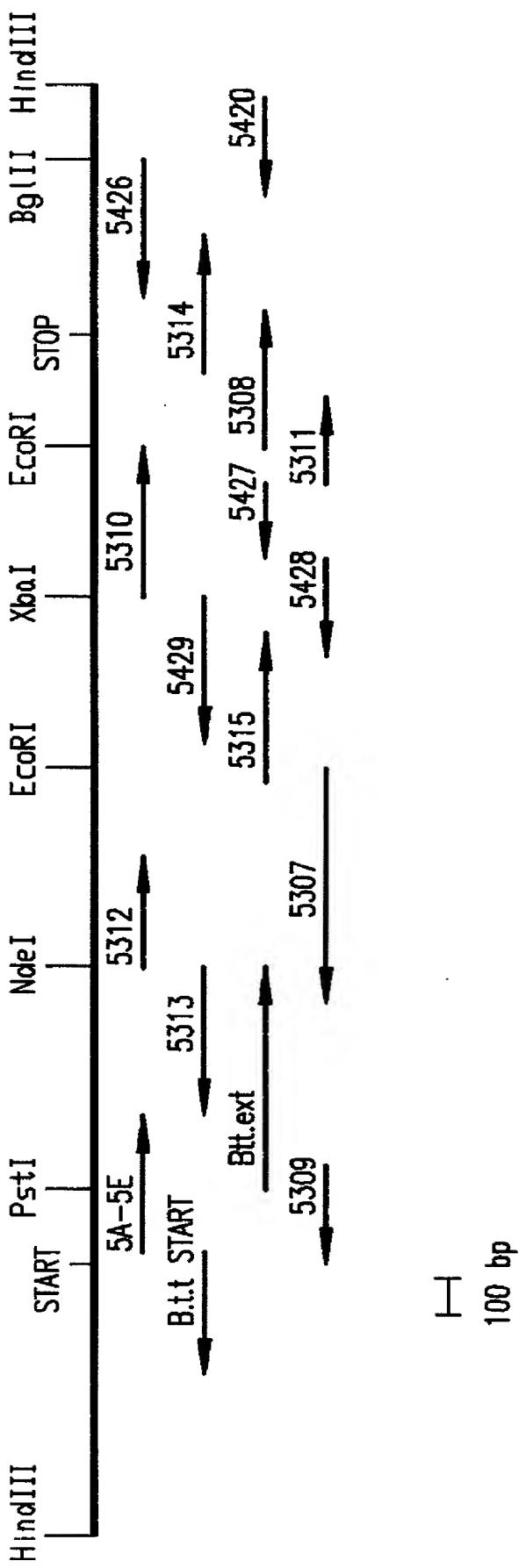


FIG.4

SEQUENCING OF THE *Bacillus Thuringiensis* var. *Tenebrionis*
INSECTICIDAL TOXIN GENE



SEQUENCE OF THE B.t.t. INSECTICIDAL TOXIN GENE AND FLANKING REGIONS

H
i
n
f
1

1 gagcgactattataatcatacatattttcTATTGGAATGATTAAGATTCCAATAGAATAG
 60 ctcgcgtataatatttagtataaaagATAACCTTACTAATTCAAGGTATCTTATC

S		F	M
M f		o	b
n a		k	o
I N		1	2
1 1			

61 TGTATAAATTATTATCTGAAAGGGAGGGATGCCTAAAAACGAAGAACATTAAAACATA
 120 ACATATTTAATAAATAGAACCTTCCTCCCTACGGATTTGCTTCTGTAAATTTGTAT

121 TATTTGACCGTCAATGGATTATGAAAAATCATTTATCAGTTGAAAATTATGTATT
 180 ATAAACGTGGCAGATTACCTAAATACTTTAGTAAAATAGTCAAACTTTAACATCAA

H		T	N
M	i M		
n	n b	a	l
I	f o	q	o
1	1 2	1	3

181 ATGATAAGAAAGGGAGGAAGAAAAATGAATCCGAACAATCGAAGTGAACATGATACAATA
 240 TACTATTCTTCCCTCTTCTTTACTTAGGCTTGTAGCTTCACTTGACTATGTTAT

START M N P N N R S E H D T I -

FIG.5A

M	M	B	N	N
a	n	a	l	l
e	t	n	a	a
2	1	1	4	3

AAA
AAACTACTGAAAATAATGAGGTGCCAACTAACCATGTTCAATATCCTTAGCGGAACT

241 TTTTGTGACTTTATTACTCCACGGTTGATTGGTACAAGTTATAGGAAATCGCCTTG 300

K T T E N N E V P T N H V Q Y P L A E T -

M	D	M	M	P
a	r	b	a	a
e	a	o	e	s
1	1	2	2	1

CCAAATCCAACACTAGAAGATTAAATTATAAAAGAGTTTAAGAACATGACTGCAGATAAT

301 -----+-----+-----+-----+-----+-----+-----+ 360
GGTTAGGTTGTGATCTCTAAATTAAATTCTCAAAAATTCTTACTGACGTCTATTA

P N P T L E D L N Y K E F L R M T A R N -

**A
I
U
1**

AATACGGAAAGCACTAGATAGCTACAACAAAAGATGTATTCAAAAGGCATTCCGTA

361 -----+-----+-----+-----+-----+-----+ 420
TTATGCCTTCGTGATCTATCGAGATGTTGTTTCTACAGTAAGTTTTCCGTAAAGGCAT

N T E A L D S S T T K D V I Q K G I S Y -

FIG.5B

S

a AMS H

HH

u vat p

ha

3 rey h

oe

A 211 1

12

/

GTAGGTGATCTCCTAGGCCTAGTAGGTTCCGTTGGAGCGCTTGTTCTTAT

421 -----+-----+-----+-----+-----+-----+ 480

CATCCACTAGAGGATCCGATCATCCAAAGGGCAAACACCTCGCGAACAAAGCAAATA

V G D L L G V V G F P F G G A L V S F Y -

D BH

M

r aa

b

a le

o

1 13

2

/

ACAAAACTTTAAATACTATTTGCCAAGTGAAGACCCGTGGAAGGTTTATGGAACAA

481 -----+-----+-----+-----+-----+-----+ 540

TGTTTAAAAATTATGATAAACCGGTTCACTTCTGGCACCTTCCGAAAATACCTTGT

T N F L N T I W P S E D P W K A F M E Q -

E S

c E a

A

A

M

o c u

I

I

a

p o 3

U

U

e

1 B A

1

1

3

GTAGAAGCATGATGGATCAGAAAATAGCTGATTATGAAAAATAAGCTTGCAGAG

541 -----+-----+-----+-----+-----+-----+ 600

CATCTTCGTAACCTACCTAGCTTTATCGACTAATACGTTTTATTCGAGAACGTCTC

V E A L M D Q K I A D Y A K N K A L A E -

FIG.5C

S

DaH

T

M

N

rua

a

b

l

a9e

q

o

a

263

1

2

3

/

TTACAGGGCCTCAAAATAATGTCGAAGATTATGTGAGTGATTGAGTTCATGGAAAAA

601 -----+-----+-----+-----+-----+-----+ 660

AATGTCCCAGAAGTTTATTACAGCTTAATAACTCACGTAACCAAGTACCGTTTTT

L Q G L Q N N V E D Y V S A L S S W Q K -

BS

sc

A

tr

l

NF

u

11

1

/

AATCCTGTGAGTTACGAAATCCACATAGCAGGGGGGATAAGAGAGCTTTCTCAA

661 -----+-----+-----+-----+-----+-----+ 720

TTAGGACACTCAAGTGTAGGTGTATCGGTCCCCGCTATTCTCTCGACAAAAGAGTT

N P V S S R N P H S Q G R I R E L F S Q -

M

n

l

1

GCAGAAAGTCATTTCTAATTCAATGCCCTCGTTGCAATTCTGGATACGGAGGTTCTA

721 -----+-----+-----+-----+-----+-----+ 780

CGTCTTCAGTAAAGCATTAAAGTTACGGAAGCAAACGTTAAAGACCTATGCTCCAAGAT

A E S H F R N S M P S F A I S G Y E V L -

FIG.5D

B	N	F
b	d	An
v	e	lu
1	1	u4
		1H

TTTCTAACACATATGCACAAGCTGCCAACACACATTATTTACTAAAAGACGCTAA
 781 -----+-----+-----+-----+-----+-----+ 840
 AAAGATTGTTGTATACTGTTGACGGTTGTGTAAATAAAAATGATTTCTGCGAGTT

F L T T Y A Q A A N T H L F L L K D A Q -
 H M M
 g b b
 a o o
 1 2 2
 ATTTATGGAGAAGAATGGGATACGAAAAAGAAGATATTGCTGAATTTATAAAAAGACAA
 841 -----+-----+-----+-----+-----+-----+ 900
 TAAATACCTCTTCTTACCCCTATGCTTTTCTTCTATAACGACTAAAATATTTCTGTT

I Y G E E W G Y E K E D I A E F Y K R Q -
 M M
 a n
 e i
 2 1
 CTAAAACCTACGCAAGAATATACTGACCATTGTGTCAAATGGTATAATGTTGGATTAGAT
 901 -----+-----+-----+-----+-----+-----+ 960
 GATTTGAATGCGTTCTTATATGACTGGTAACACAGTTACCATATTACAACCTAATCTA

L K L T Q E Y T D H C V K W Y N V G L D -
 H
 i
 n
 f
 1
 AAATTAAGAGGTTCATTTATGAATCTTGGGTAAACCTTAACCGTTATCGCAGAGAGATG
 961 -----+-----+-----+-----+-----+-----+ 1020
 TTAAATTCTCAAGTAGAATACTAGAACCCATTGAAATTGGCAATAGCGTCTCTAC

K L R G S S Y E S W V N F N R Y R R E M -

FIG.5E

ACATTAACAGTATTAGATTAAATTGCACTATTCCATTGTATGATGTCGGCTATAACCCA
 1021 -----+-----+-----+-----+-----+-----+ 1080
 TGTAATTGTCATAATCTAAATTAAACGTGATAAAGGTAAACACTACAAGCCGATATGGGT

T L T V L D L I A L F P L Y D V R L Y P -

S	H	H
aX	i	i
uh	n	n
3o	f	c
A2	1	2

/

AAAGAAGTTAAAACCGAATTAACAAGAGACGTTAACAGATCCAATTGTCGGAGTCAC
 1081 -----+-----+-----+-----+-----+-----+ 1140
 TTTCTTCAATTTGGCTTAATTGTTCTCTGAAAATTGTCTAGGTTAACAGCCTCAGTTG

K E V K T E L T R D V L T D P I V G V N -

DM	AT.
ds	sq
et	uq
12	21

/

AACCTTAGGGCTATGGAACAACCTCTCTAATATAGAAAATTATATTGAAAACCACAT
 1141 -----+-----+-----+-----+-----+-----+ 1200
 TTGGAATECCCCGATAACCTTGTGGAAGAGATTATATCTTTAATATAAGCTTTGGTGTA

N L R G Y G T T F S N I E N Y I R K P H -

E	BS
C	T N sc
O	h l fr
R	a a NF
I	1 4 11

/

CTATTTGACTATCTGCATAGAATTCAATTACACGCGGTTCAACCAAGGATATTATGGA
 1201 -----+-----+-----+-----+-----+-----+ 1260
 GATAAAACTGATAGACGTATCTTAAGTTAAAGTGTGCGCCAAGGTTGGTCTATAATACCT

L F D Y L H R I Q F H T R F Q P G Y Y G -

FIG.5F

H	S		S
i	Aa H	M	a
n	v u p	a	u
f	a9 a	e	3
1	26 2	1	A
	/		

1261 AATGACTTTCAATTATTGGTCCGTAATTATGTTCACTAGACCAAGCATAGGATCA
 TTACTGAGAAAGTTAATAACCAGGCCATTAAATACAAAGTTGATCTGGTTCGTATCCTAGT 1320

N D S F N Y W S G N Y V S T R P S I G S -

E	P	
c	f	R
o	i	s
p	m	a
1	1	1

1321 AATGATATAATCACATCTCATTCTATGGAAATAATCCAGTGAACCTGTACAAAATTAA
 TTACTATATTAGTAGAGGTAAGATAACCTTTATTTAGGTCACTGGACATGTTTAAAT 1380

N D I I T S P F Y G N K S S E P V Q N L -

E		H
c		a
o		e
p		3
1		

1381 GAATTTAATGGAGAAAAAGTCTATAGAGCCGTAGCAAATACAATCTTGCCTCTGGCG
 CTTAAATTACCTCTTTCAAGATATCTCGGCATCGTTATGTTAGAACGCCAGACCGGC 1440

E F N G E K V Y R A V A N T N L A V W P -

FIG.5G

M	S
a	Ba
e	cu
3	13
	1A
	/

TCCGCTGTATATTCAAGGTGTTACAAAGTGGAAATTAGCCAATATAATGATCAAACAGAT
 1441 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1500
 AGGCACATATAAGTCACAATGTTTACCTTAAATCGTTATATTACTAGTTGTCTA

S A V Y S G V T K V E F S Q Y N D Q T D -

R	H	R	H
s	i	i	HT
a	n	b	AP
1	f	aa	i
	1 1	uu	v
		11	12
		/	1
		/	/

GAAGCAAGTACACAAACGTACGACTCAAAAGAAAATGTTGGCGGGTCAGCTGGGATTCT
 1501 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1560
 CTTCGTTCATGTGTTGCATGCTGAGTTTCTTACAACCGCGCCAGTCGACCTAAGA

E A S T Q T Y D S K R N V G A V S W D S -

S				
CaT	M	XM	M	N
lua	n	ba	n	l
a3q	l	ae	l	a
1A1	1	11	1	3
/				

ATCGATCAATTGCCCTCAGAAACACAGATGAACCTCTAGAAAAGGGATATAGCCATCAA
 1561 -----+-----+-----+-----+-----+-----+-----+-----+-----+ 1620
 TAGCTAGTTAACGGAGGTCTTGTTGTCTACTTGGAGATCTTTCCCTATATCGGTAGTT

I D Q L P P E T T D E P L E K G Y S H Q -

FIG.5H

M	H
n	iH
I	np
1	ca
	21

/

CTCAATTATGTAATGTGCTTTAATGCAGGGTAGTAGAGGAACAATCCCAGTGTTAATC

1621 -----+-----+-----+-----+-----+-----+ 1680
GAGTTAACATTACACGAAAAATTACGTCCCATCATCTCCTGTTAGGGTCACAATTGA

L N Y V M C F L M Q G S R G T I P V L T -

A	N	H
C	i	AT
C	l	nsq
1	a	f uq
	3	1 21

/

TGGACACATAAAAGTGTAGACTTTTTAACATGATTGATTGCGAAAAAAATTACACAACCTT

1681 -----+-----+-----+-----+-----+-----+ 1740
ACCTGTGTATTTCACATCTGAAAAAAATTGTACTAACTAAGCTTTTTAATGTGTTGAA

W T H K S V D F F N M I D S K K I T Q L -

M	B	P S
a	s	ADpAMaS M
e	p	vruvaut n
3	M	aaMre9y l
	1	2212161 1

// //

CCGTTAGTAAAGGCATATAAGTTACAATCTGGTGCTTCCGTTGTCGAGGTCTAGGTTT

1741 -----+-----+-----+-----+-----+-----+ 1800
GGCAATCATTCGTATATTCAATGTAGACCACGAAGGCAACAGCGTCCAGGATCCAAA

P L V K A Y K L Q S G A S V V A G P R F -

FIG.5I

E
C
O
R
V

F
n
u
4
H

M
a
e
3

ACAGGGAGGAGATATCATTCAATGCACAGAAAATGGAAGTGCAGCACTATTTACGTTACA

1801 -----+-----+-----+-----+-----+ 1860
TGTCTCTCTATAGTAAGTTACGTGTCTTACCTCACGCCGTTGATAATGCAATGT

T G G D I I Q C T E N G S A A T I Y V T -

	E					
H	R	F	T	AM	c	D
p	s	o	a	la	o	d
q	a	k	q	ue	R	e
2	1	1	1	11	1	1

CCGGATGTGTCGTACTCTCAAAAATATCGAGCTAGAATTCAATTGCTTACATCTAG

1861 -----+-----+-----+-----+-----+ 1920
GGCCTACACAGCATGAGAGTTTTATAGCTCGATCTTAAGTAATACGAAGATGTAGAGTC

P D V S Y S Q K Y R A R I H Y A S T S Q -

	B				
D	B	Ns			T
d	a	lp			a
e	n	a1			q
1	1	42			1

ATAACATTACACTCAGTTAGACGGGGACCCATTAACTCAAACTATTTCGATAAAACG

1921 -----+-----+-----+-----+-----+ 1980
TATTGTAAATGTGAGTCAAATCTGCCCGTGGTAAATTAGTTATGATAAAGCTATTTGC

I T F T L S L D G A P F N Q Y Y F D K T -

ATAAATAAAGGAGACACATTAACGTATAATTCAATTAGCAAGTTCAGCACACCA

1981 -----+-----+-----+-----+-----+ 2040
TATTATTCTCTGTGTAAATTGCATATTAAGTAAATTAAATGTTCAAAGTCGTGTGGT

I N K G D T L T Y N S F N L A S F S T P -

FIG.5J

AT H AM
sa g ha
uq q ae
21 1 23
/

TTCGAATTATCAGGGAATAACTACAAATAGGCCTCACAGGATTAAGTGCTGGAGATAAA
2041 -----+-----+-----+-----+-----+-----+-----+ 2100
AAGCTTAATAGTCCCTTATTGAATGTTATCCGAGTGTCTAATTACGACCTCTATTT

F E L S G N N L Q I G V T G L S A G D K -

X M
m a
n e
1 1

GTTTATATAGACAAAATTGAATTATTCCAGTGAATTAAATTAACTAGAAAGTAAAGAAG
2101 -----+-----+-----+-----+-----+-----+-----+ 2160
CAAATATATCTGTTTAACCTAACATAAGGTCACTTAATTAAATTGATCTTCATTTCTTC

V Y I D K I E F I P V N x STOP

M M
a b
e o
3 2

TAGTGACCATCTATGATAGTAAGCAAAGGATAAAAAAATGAGTTCATAAATGAATAACA
2161 -----+-----+-----+-----+-----+-----+-----+ 2220
ATCACTGGTAGATACTATCATTGTTCTATTTTTACTCAAGTATTTACTTATTGT

M
b
o
2

TAGTGTTCTCAACTTCTGTTTGAAGGTAGATGAAGAACACTATTTTATTTCAA
2221 -----+-----+-----+-----+-----+-----+-----+ 2280
ATCACAAAGTTGAAAGCGAAAAACTTCCATCTACTTCTGTGATAAAAATAAGTTT

FIG.5K

<p>D r a 1</p> <p>2281</p>	<p>D r a 1</p>	
--	----------------------------	--

ATGAAGGAAGTTTAAATATGAAATCATTTAAAGGGAAACAATGAAAGTAGGAAATAAGTC
 TACCTCCTCAAAATTATACATTAGTAATTCCTGTACTTCATCCTTATTCAAG

<p>S s p 1</p> <p>2341</p>		
--	--	--

ATTATCTATAACAAAATAACCATTTATATAGCCAGAAATGAATTATAATATTAATCTT
 TAATAGATATTGTTTATTGGTAAAAATATCGGTCTTACTTAATATTATAATTAGAA

<p>H A l u 1</p> <p>2401</p>	<p>H D d e 1</p>	<p>iH ng fa 11</p>	<p>S S p 1</p>	
--	----------------------------------	--------------------------------	----------------------------	--

TTCTAAATTGACGTTTCTAACGTTCTATAGCTCAAGACGETTAGAATCATCAATAT
 AAGATTTAAGTGAAAAGAATTGCAAGATATCGAAGTTCTGCGAATCTTAGTAGTTATA

<p>A A T</p> <p>C l a</p> <p>C u q</p> <p>1 1 1</p> <p>2461</p>	<p>H</p>	<p>i</p>	<p>B</p>	
---	----------	----------	----------	--

TTGTATACAGAGCTGTTGTTCCATCGAGTTATGTCCATTGATTGCTAATAGAACAA
 AACATATGTCCTGACAACAAAGGTAGCTCAATACAGGGTAAACTAAGCGATTATCTGTT

FIG.5L

S

aX

uh

3o

A2

//

GATCTTATTTGTTATAATGATTGGTTGCATAAGTATGGCGTAATTATGAGGGCTT

2521 -----+-----+-----+-----+-----+-----+ 2580
CTAGAAATAAAAGCAATATTACTAACCAACGTATTCATACCGCATTAAACTCCCGAAA

TCTTTCATCCAAAAGCCAAGTGTATTCTCTGTA

2581 -----+-----+-----+----- 2615
AGAAAAGTAGGTTTCGGTTCACATAAAGAGACAT

FIG.5M

B.t.t. PROTEINS - NATIVE & <u>E.coli</u> CLONES					
BAND No.	MW (Kd)	NATIVE B.t.t.	pMON5436	E.coli CLONES pMON5456	pMON5460 pMON5450
1	73	—	—	—	—
2	71	—			
.					
3,3'	67	—	—	—	
4	66	—			

DIAGRAM OF B.t.t. PROTEINS. B.t.t. PROTEINS PRODUCED BY *Bacillus Thuringiensis* var. *Tenebrionis* and *E.coli* JM101 (pMON5436, pMON5456, pMON5450, pMON5460) WERE RESOLVED ON 9% SDS-PAGE AND THE RESPECTIVE PATTERNS ARE SHOWN.

FIG.6

N-TERMINI OF B.t.t. PROTEINS

1 2 3 3'
1 MNPNNRSEHD TIKTENNEV PTNHVQYPLA ETPNPTLEDL NYKEFLRMTA
4
51 DNNTEALDSS TTKDVHQKGI SVVGDLLGVV GFPFGGALVS FYTNFLNTIW
101 PSED PWKA FM EQVE ALMD QK IAD YAK NKA L AEL QGL QNN V EDY VSAL SSW
151 QKNP VSS RNP HSQGR IRE LF SQA ESH FRNS MPS FAIS GYE VL FL TT Y AQA
201 ANTHL FLL KD AQI YGE EW GY EK DIA EFP YK RQL KLT QE YT DH CV KW NVG
251 LD KL RG SS YE SW NF NR Y RR EM TL TV LD L I AL FPL YD V RL YP KE VK T EL T

N-TERMINI OF THE UNIQUE B.t.t. PROTEINS PRODUCED
IN EITHER B.t.t. AND/OR E. COLI WERE DETERMINED BY
AMINO ACID SEQUENCING. THE ARROWS AND ASSOCIATED
NUMBERS CORRESPOND TO THE FIRST AMINO ACID OF THE
PROTEINS DESCRIBED IN FIG. 6.

FIG.7

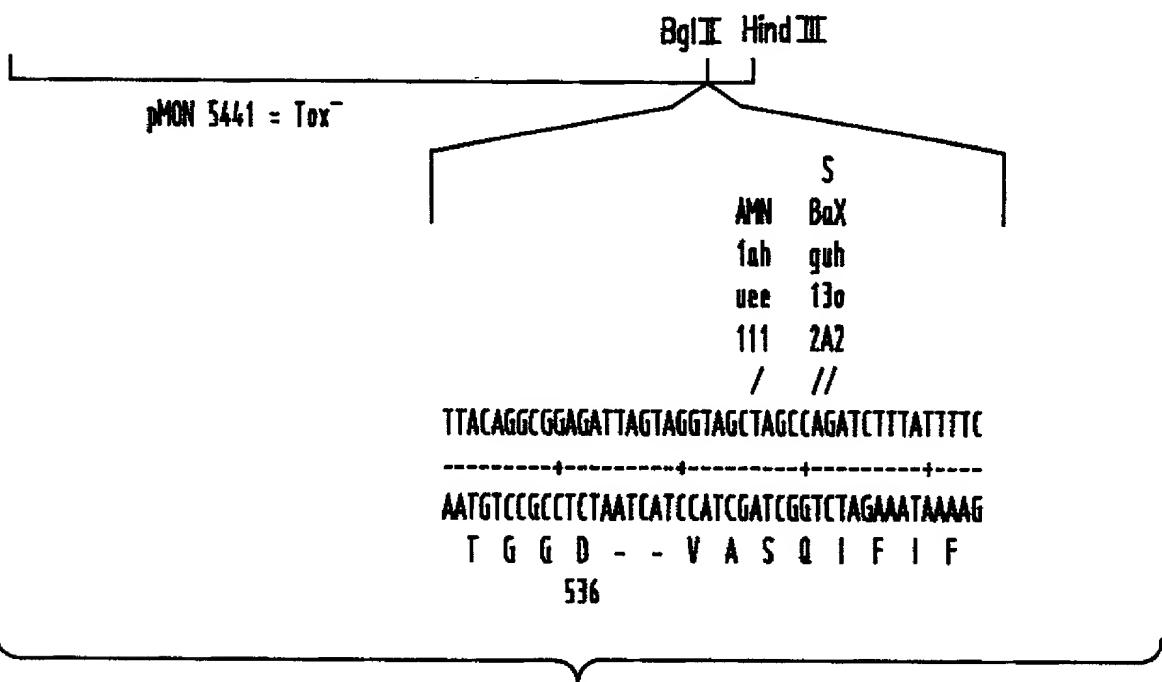
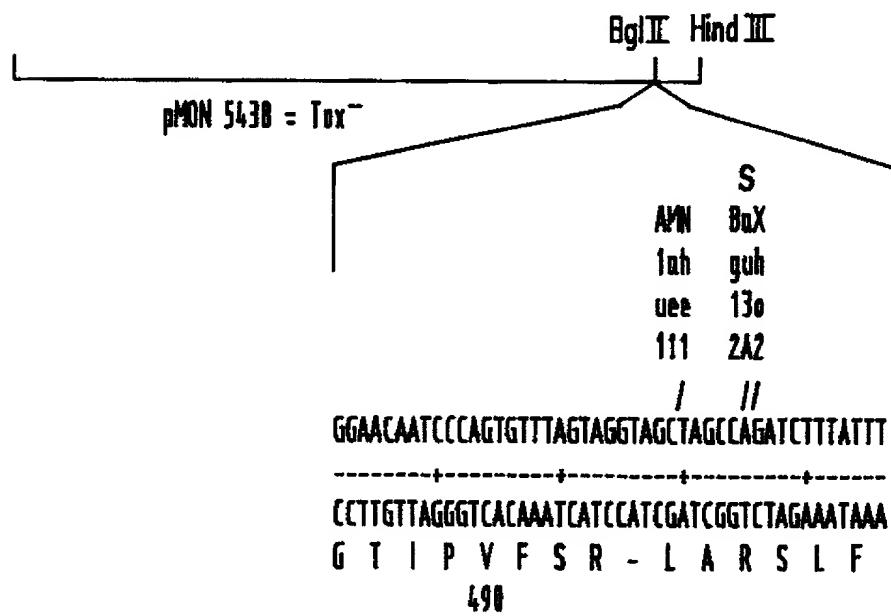
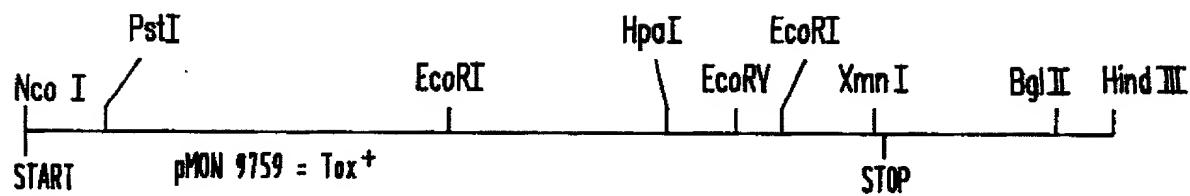


FIG.8A

pMON 5449 = Tox -

BglII HindIII

D	H	AMN	S
d	a	tah	BeX
e	e	uee	guh
i	i	ii	13o
		/	2A2
		//	

CTCAGTTAGACGGGGTAGTAGGTAGCTAGCCAGATCTTATT

GAGTCAAATCTGCCCGATEATCCATGATGGTCTAGAAATAAA
L S L D G A S R - L A R S L F

582

pMON 5448 = Tox -

BglII HindIII

AMN	S
tah	BeX
uee	guh
ii	13o
/	2A2
//	

GTTTATATAGACAAAATTGAATTAGTAGGTAGCTAGCCAGATCTTATT

CAAATATATCTGTTTACTTAAATCATCCATGATGGTCTAGAAATAAA
V Y I D K I E F S R - L A R S L F

640

THE INSERTS SHOW THE ACTUAL AMINO ACID
SEQUENCE OF THE ALTERED B.t.t. PROTEINS.

FIG.8B

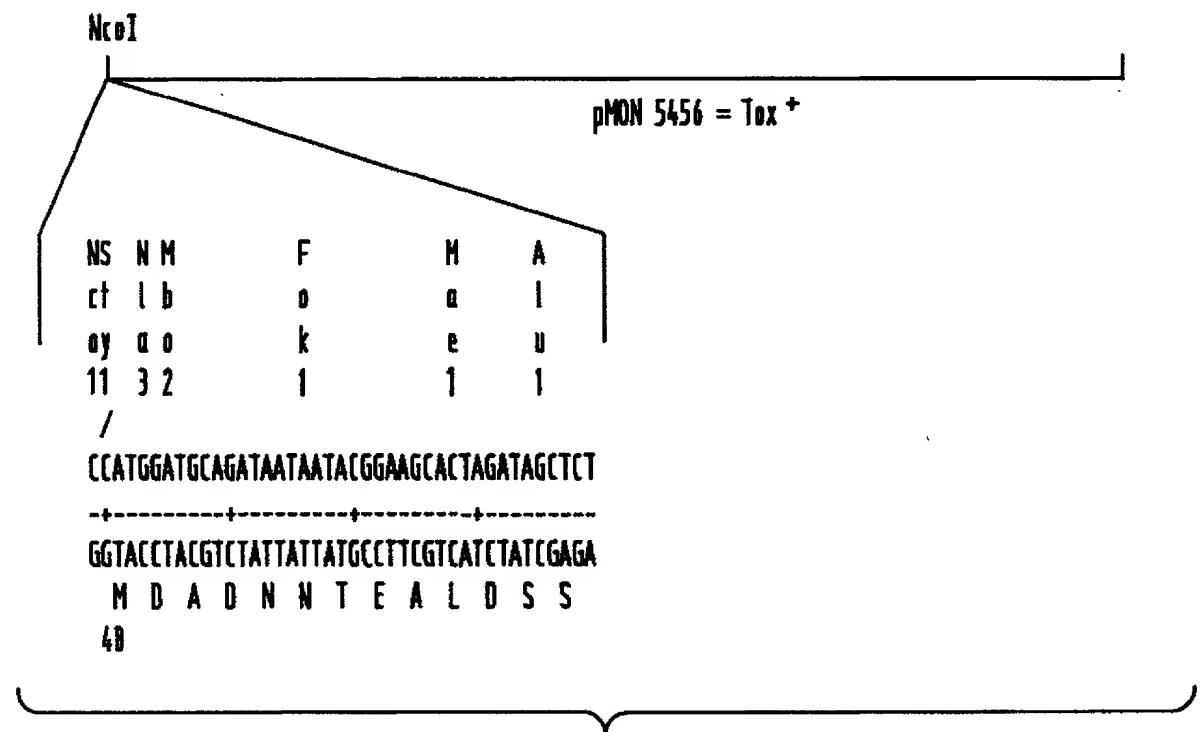
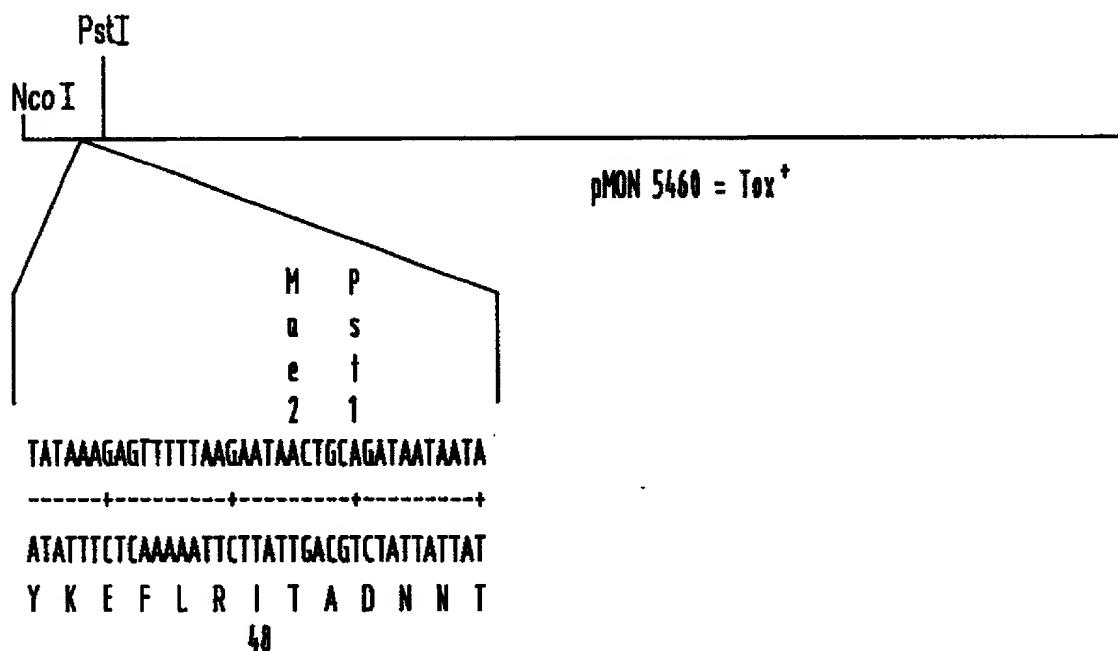
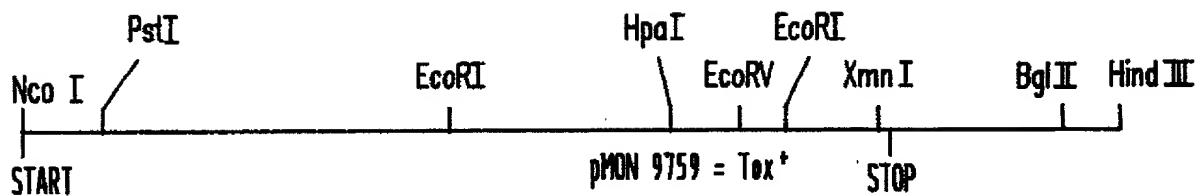
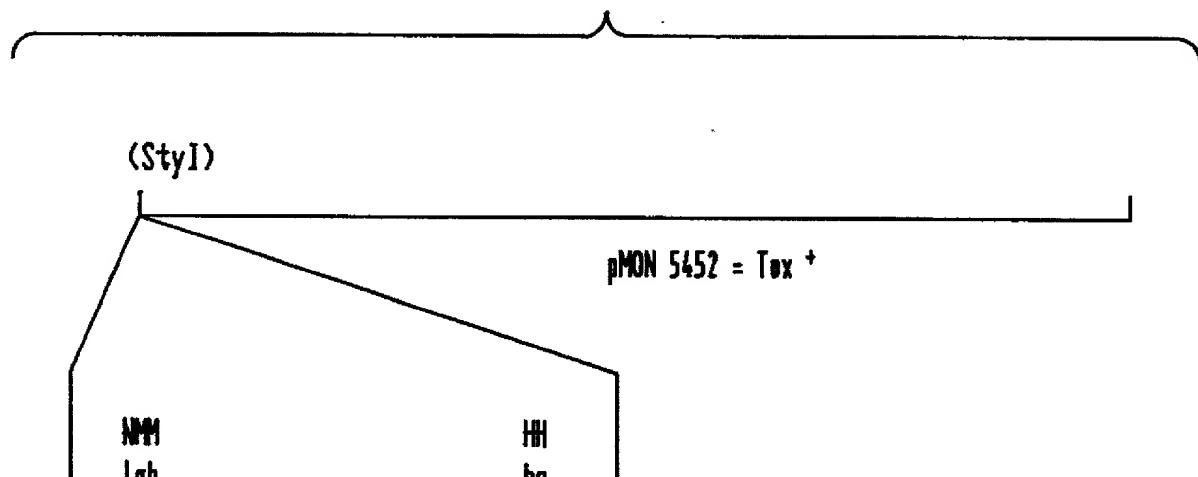


FIG.9A



CCATGCTAGGAGTAGGTTCGGTTGTGGAGGGTTC
 +-----+-----+-----+-----+
 GGTACGATECTCATCATCAAGGGCAACACCTCGCGAAC
 M L G V V G F P P V E R L
 77



CCATGGCAATTGGCCAAGTGAAGAC
 -----+-----
 GGTACCGTTAACCGGTTCACTTCG
 M A I W P S E D
 99

THE INSERTS SHOW THE ACTUAL AMINO ACID
 SEQUENCE OF THE ALTERED B.T.f. PROTEINS.

FIG.9B

SUMMARY OF N-TERMINUS AND C-TERMINUS TRUNCATIONS OF THE B.t.t. TOXIN

1 MDPNNRSEHD TIKTENNEV PTNHVQYPLA ETPNPTLEDL NYKEFLRMTA
▲ 5456+

51 DNNTEALDSS TTKDVIQKGI SVVGDLLGVV GFPFGGALVS FYTNFLNTIW
▲ 5452+ ▲ 5467-

101 PSED PWKA FM EQVE ALMDQK IADYAKN KAL AELO QGLQNNV EDYV SALSSW

151 QKNPVSSRNP HSQGRIRELF SQAESHFRNS MPSFAISGYE VLFLT TYAQA

201 ANTHLFL LKD AQIYGE EWGY EKEDIAEF YK RQLKL TQE YT DHCV KWYN VG

251 LDKL RGSSYE SWVN FNRY RR EM TLTV LDLI ALFPL YD VRL YPK EVKT ELT

301 RDVL TDPI YG VNNL RGY GTT FSNI ENYIRK PHLFDYLHRI QFHTRF QPGY

351 YGNDSF NYWS GNYVSTRPSI GSNDI ITSPF YGNKS SEP VQ NLEFN GEKVY

401 RAVANTNL AV WPSAVYSGVT KVEFSQYNDQ TDEASTQTYD SKRN VGA VSW

451 DSIDQ LP PET TDEPLEKGYS HQLNYVMCFL MQGSRG TIPV LTWTHK SVDF
▲ 5438-

501 FNMIDS KKIT QLPLV KAYKL QSGASVVA GP RFTGGDIIQC TENG SAATI Y
▲ 5441-

551 VTPDV SYSQK YRARIHYAST SQITFTLSLD GAPFNQYYFD KTINKGDTLT
▲ 5449-

601 YNSFNL ASFS TP FELSGNNL QIGVTGLSAG DKVYIDKIEF IPVN
▲ 5448-

FIG.10

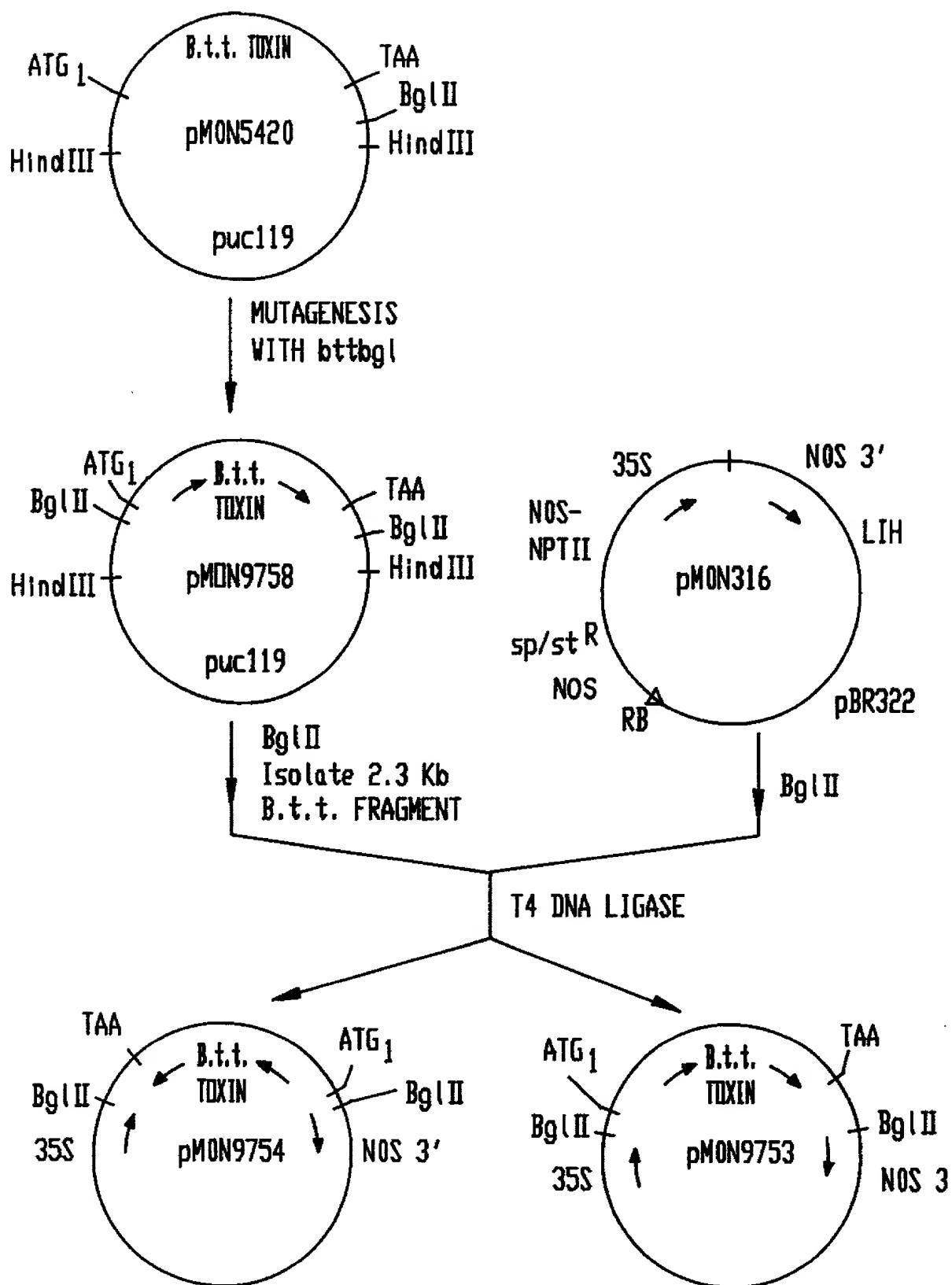


FIG.11

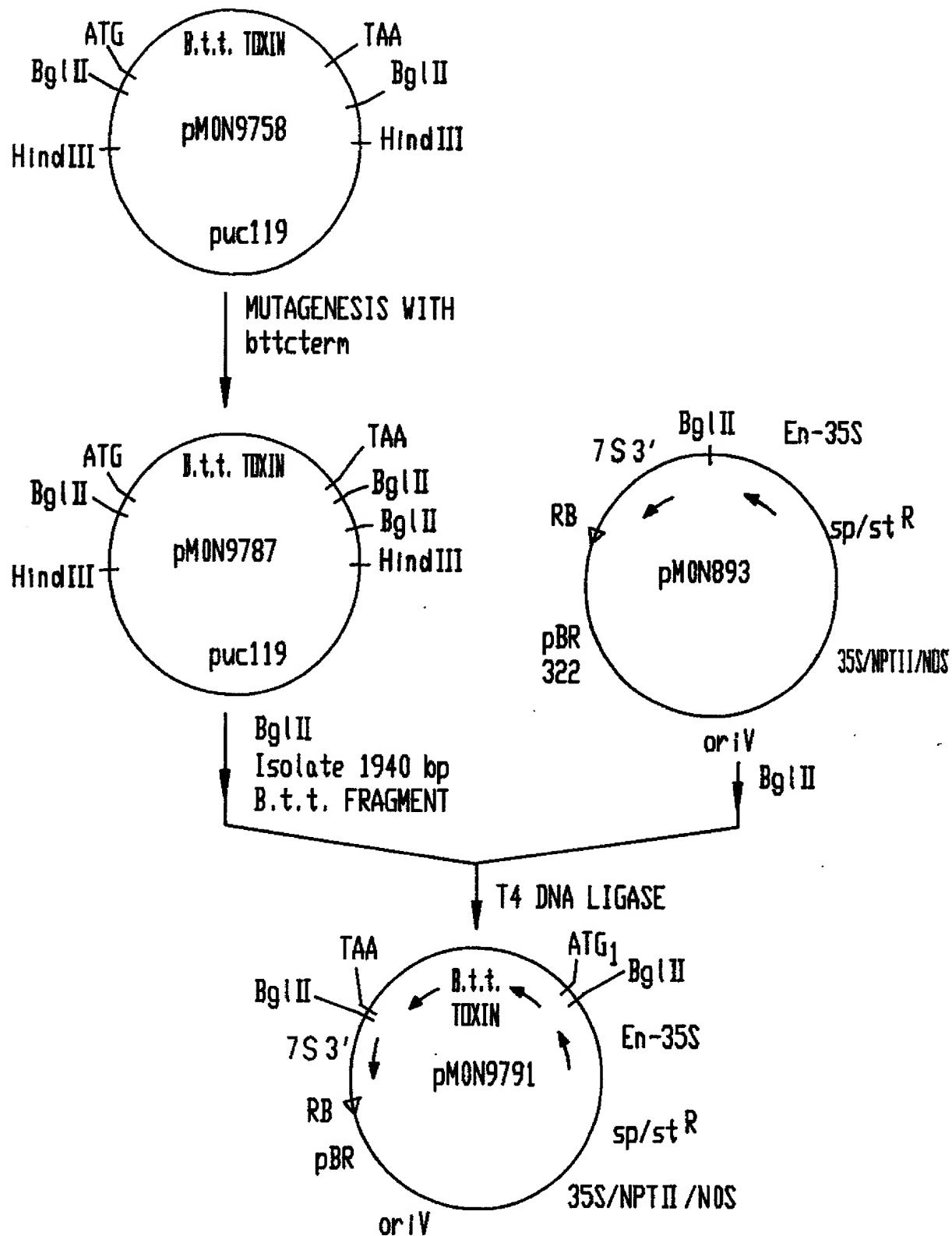


FIG.12

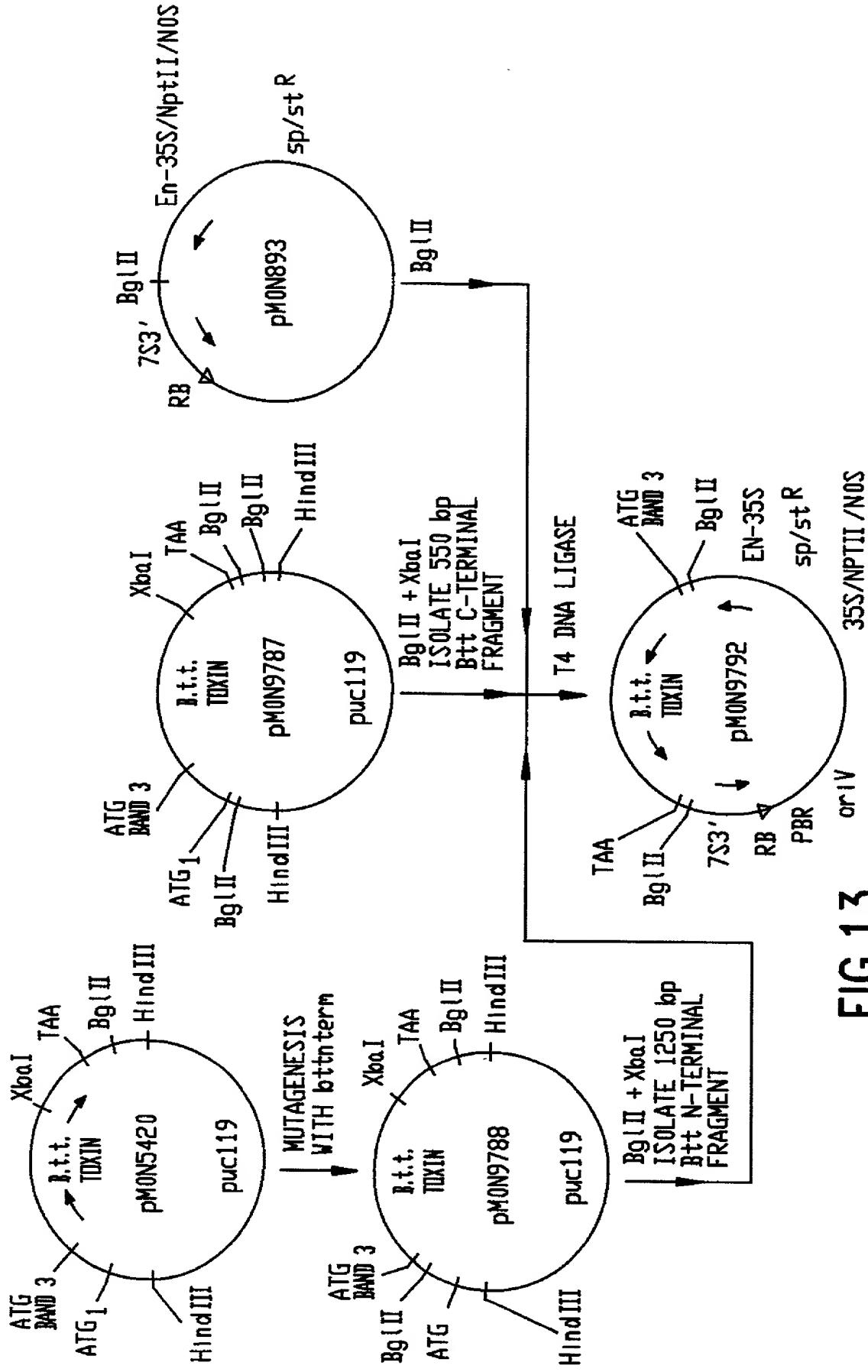


FIG. 13

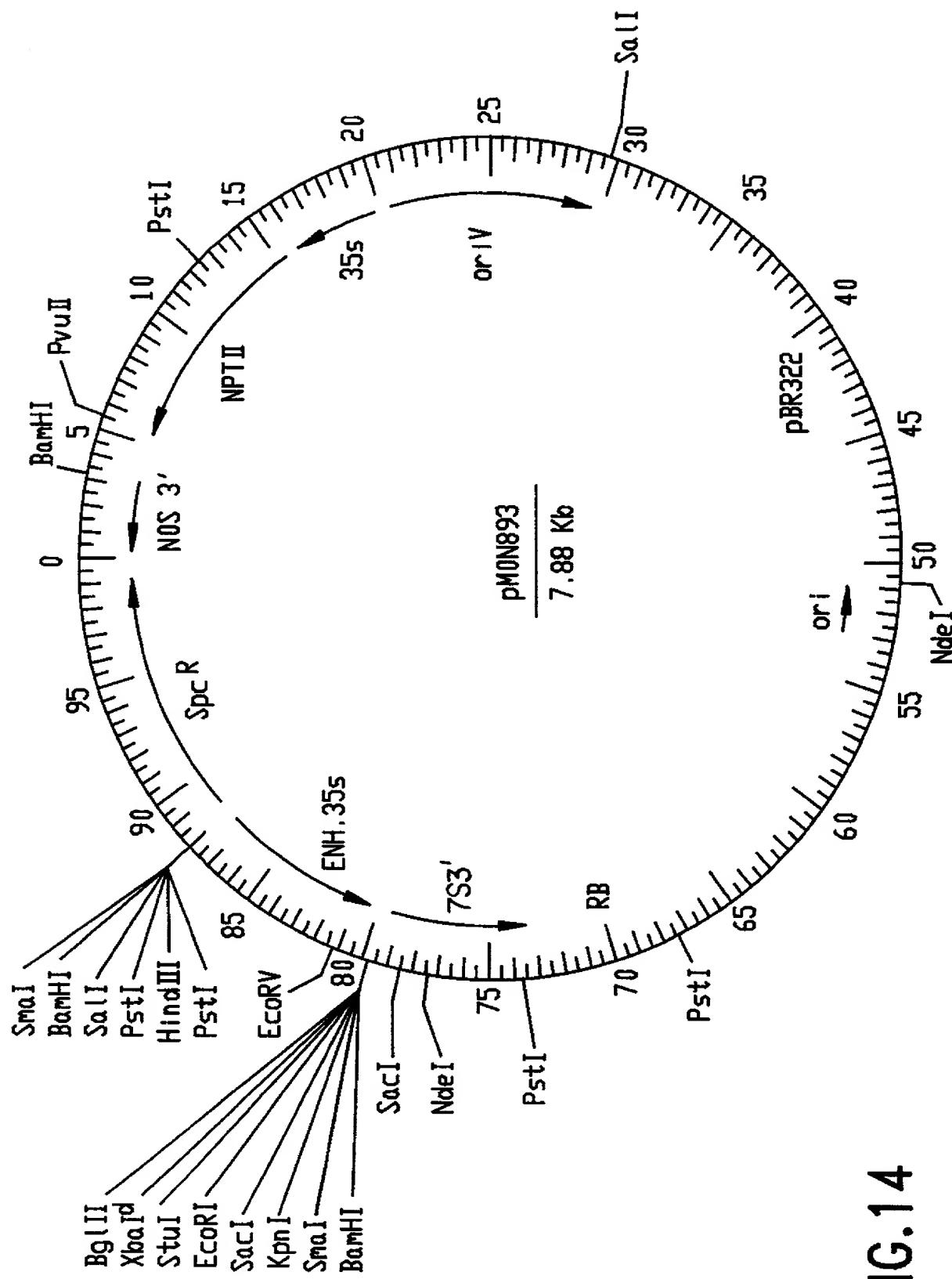


FIG. 14

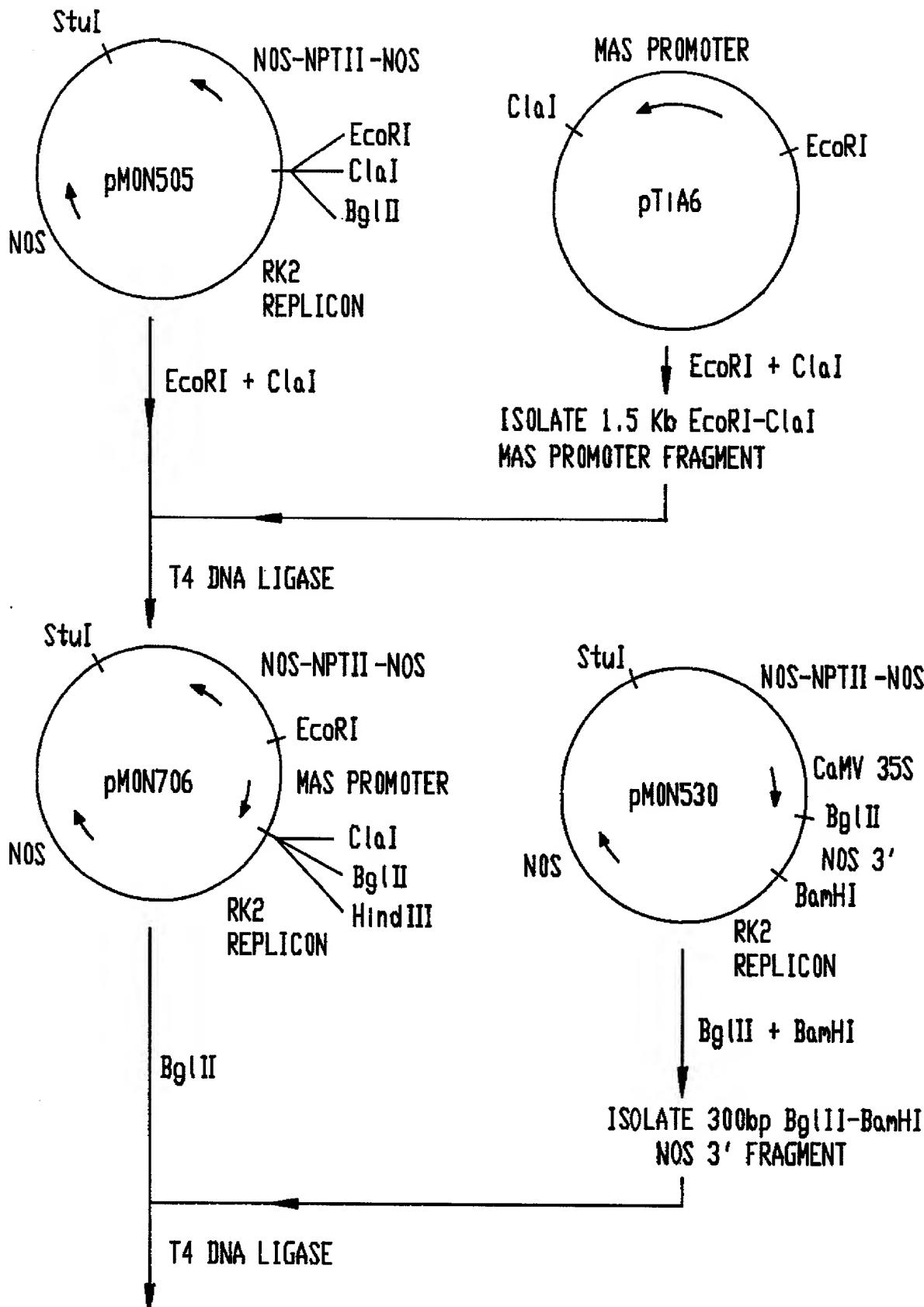


FIG.15A

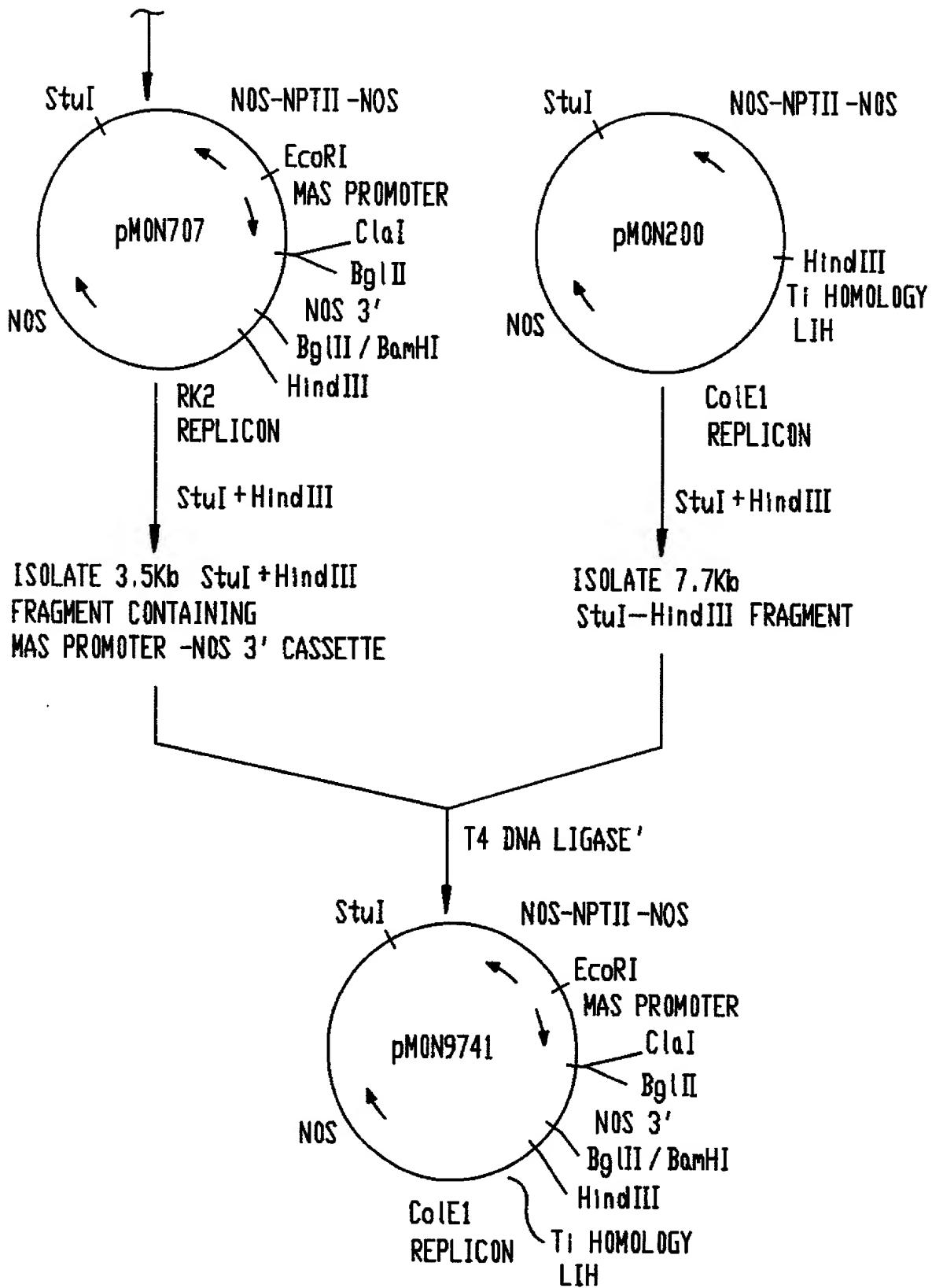


FIG.15B

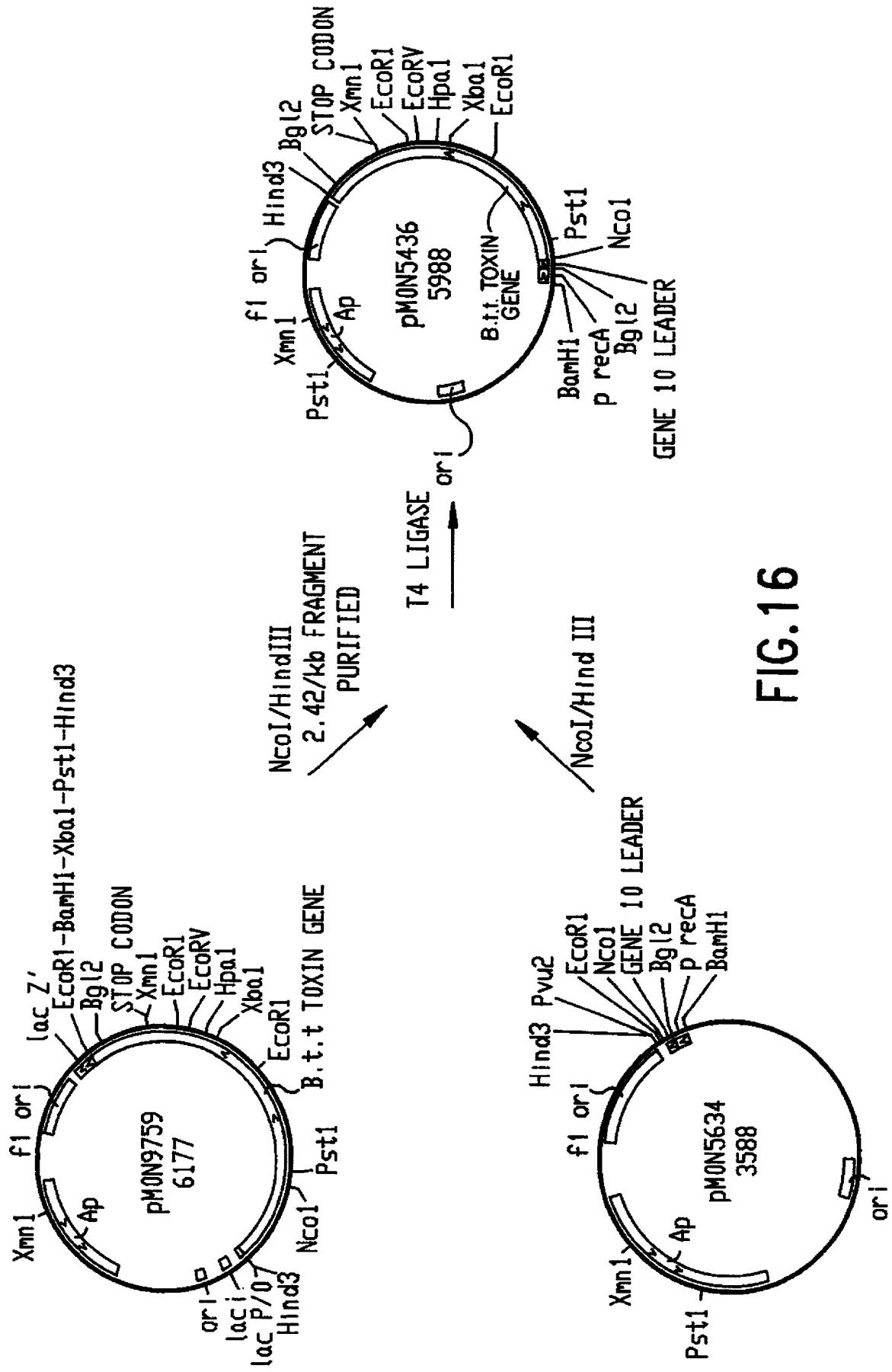


FIG. 16

T- DNA REGION IN AGROBACTERIUM ACO

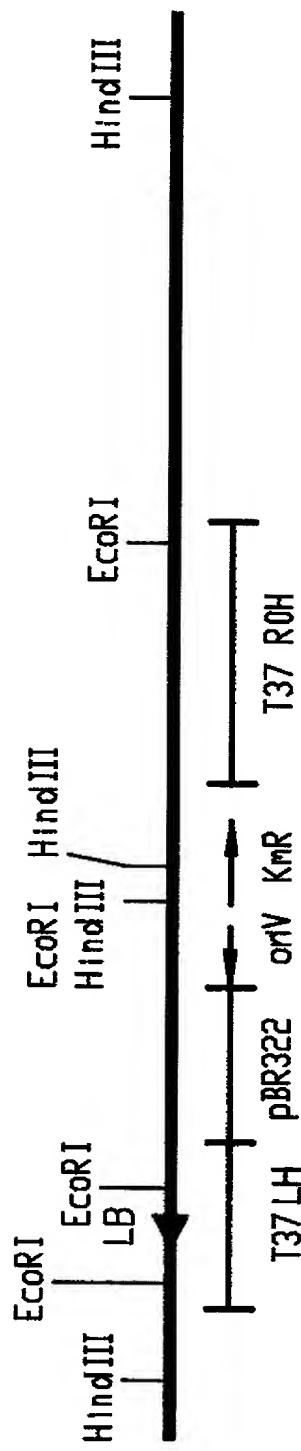


FIG. 17

DNA SEQUENCE FOR THE ENHANCED α MY35S PROMOTER
USED IN THE PREPARATION OF pMONB93

*
5' -AAGCTTGAT GCCTGCAGGT CCGATG[GAG ACTTTCAAC AAAGGGTAAT 50
ATCCGGAAAC CTCCCTGGAT TCCATTGCC AGCTATETGT CACTTTATTG 100
TGAAGATA[G]T GGAAAAGGAA GGTGGCTCCT ACAAAATGCCA TCATTCGGAT 150
AAAGGAAAGG CCATCGTGA AGATGCCTCT GCCGACAGTG GTCCCAAAGA 200
TGGACCCCCA CCCACGAGGA GCATCGTGA AAAAGAAGAC GTTCCAACCA 250
CGTCTTCAAA GCAAGTGGAT TGATGTGA[G] GTCCGGAT[G] AGACTTTCA 300
ACAAAGGGTA ATATCCGGAA ACCTCCCTGG ATTCCATTGC CCAGCTATCT 350
GTCACTTAT TGTGAAGATA GTGGAAAAGG AAGGTGGCTC CTACAAATGC 400
CATCATTGCG ATAAAGGAAA GGCCATCGT GAAGATGCC CTGCCGACAG 450
TGGTCCAAA GATGGACCCC CACCCACGAG GAGCATCGT GAAAAAGAAG 500
ACGTTCAAAC CACGTCTCA AAGCAAGTGG ATTGATGTGA [ATCTCCACT 550
GACGTAAGGG ATGACGCACA ATCCCACTAT CCTTCGCAAG ACCCTTCCTC 600
TATATAAGGA AGTCATTTC ATTTGGAGAG GACACGCTGA CAAGCTGACT 650
CTAGCAGATC T - 3' 661

* BRACKETED SEQUENCE INDICATED DUPLICATED ENHANCER SEQUENCE

FIG.18